

Zhixi Su

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,916
citations

567281

15
h-index

276875

41
g-index

42
all docs

42
docs citations

42
times ranked

3164
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic evaluation of the effect of polyadenylation signal variants on the expression of disease-associated genes. <i>Genome Research</i> , 2021, 31, 890-899.	5.5	8
2	Ancestral transcriptome inference based on RNA-Seq and ChIP-seq data. <i>Methods</i> , 2020, 176, 99-105.	3.8	5
3	The Impact of DNA Methylation Dynamics on the Mutation Rate During Human Germline Development. <i>C3: Genes, Genomes, Genetics</i> , 2020, 10, 3337-3346.	1.8	22
4	Global Analysis of Gene Expression Profiles Provides Novel Insights into the Development and Evolution of the Large Crustacean <i>Eriocheir sinensis</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 443-454.	6.9	5
5	Comparative Transcriptome Analyses Reveal the Role of Conserved Function in Electric Organ Convergence Across Electric Fishes. <i>Frontiers in Genetics</i> , 2019, 10, 664.	2.3	4
6	DeepHLApan: A Deep Learning Approach for Neoantigen Prediction Considering Both HLA-Peptide Binding and Immunogenicity. <i>Frontiers in Immunology</i> , 2019, 10, 2559.	4.8	84
7	Integrative Analysis of Somatic Mutations in Non-coding Regions Altering RNA Secondary Structures in Cancer Genomes. <i>Scientific Reports</i> , 2019, 9, 8205.	3.3	14
8	Olfactomedin domain-containing proteins: evolution, functional divergence, expression patterns and damaging SNPs. <i>Molecular Genetics and Genomics</i> , 2019, 294, 875-885.	2.1	9
9	TSNAdb: A Database for Tumor-specific Neoantigens from Immunogenomics Data Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 276-282.	6.9	97
10	Brownian model of transcriptome evolution and phylogenetic network visualization between tissues. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 34-39.	2.7	5
11	TSNAD: an integrated software for cancer somatic mutation and tumour-specific neoantigen detection. <i>Royal Society Open Science</i> , 2017, 4, 170050.	2.4	80
12	Phosphotyrosine signalling and the origin of animal multicellularity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170681.	2.6	7
13	Paralog-divergent Features May Help Reduce Off-target Effects of Drugs: Hints from Glucagon Subfamily Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 246-254.	6.9	2
14	Mutation-profile-based methods for understanding selection forces in cancer somatic mutations: a comparative analysis. <i>Oncotarget</i> , 2017, 8, 58835-58846.	1.8	11
15	<scp>TreeExp</scp> 1.0: R Package for Analyzing Expression Evolution Based on RNA-Seq Data. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2016, 326, 394-402.	1.3	19
16	Advances in Computational Genomics. <i>BioMed Research International</i> , 2015, 2015, 1-2.	1.9	0
17	The Evolutionary Panorama of Organ-Specifically Expressed or Repressed Orthologous Genes in Nine Vertebrate Species. <i>PLoS ONE</i> , 2015, 10, e0116872.	2.5	5
18	Effect of Duplicate Genes on Mouse Genetic Robustness: An Update. <i>BioMed Research International</i> , 2014, 2014, 1-13.	1.9	7

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19	Age distribution patterns of human gene families: divergent for Gene Ontology categories and concordant between different subcellular localizations. <i>Molecular Genetics and Genomics</i> , 2014, 289, 137-147.	2.1	3
20	Asymmetric Evolution of Human Transcription Factor Regulatory Networks. <i>Molecular Biology and Evolution</i> , 2014, 31, 2149-2155.	8.9	8
21	A note on gene pleiotropy estimation from phylogenetic analysis of protein sequences. <i>Journal of Systematics and Evolution</i> , 2013, 51, 365-369.	3.1	3
22	Phylogenomic Distance Method for Analyzing Transcriptome Evolution Based on RNA-seq Data. <i>Genome Biology and Evolution</i> , 2013, 5, 1746-1753.	2.5	16
23	An Update of DIVERGE Software for Functional Divergence Analysis of Protein Family. <i>Molecular Biology and Evolution</i> , 2013, 30, 1713-1719.	8.9	171
24	Identification of Functional Mutations in GATA4 in Patients with Congenital Heart Disease. <i>PLoS ONE</i> , 2013, 8, e62138.	2.5	49
25	Revisit on the evolutionary relationship between alternative splicing and gene duplication. <i>Gene</i> , 2012, 504, 102-106.	2.2	20
26	Histone modification pattern evolution after yeast gene duplication. <i>BMC Evolutionary Biology</i> , 2012, 12, 111.	3.2	9
27	Functional complementation between transcriptional methylation regulation and post-transcriptional microRNA regulation in the human genome. <i>BMC Genomics</i> , 2011, 12, S15.	2.8	52
28	Comment on "Positive Selection of Tyrosine Loss in Metazoan Evolution". <i>Science</i> , 2011, 332, 917-917.	12.6	13
29	Conservation and divergence of DNA methylation in eukaryotes. <i>Epigenetics</i> , 2011, 6, 134-140.	2.7	65
30	A preliminary analysis of gene pleiotropy estimated from protein sequences. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2010, 314B, 115-122.	1.3	31
31	Differences in duplication age distributions between human GPCRs and their downstream genes from a network prospective. <i>BMC Genomics</i> , 2009, 10, S14.	2.8	5
32	Simultaneous expansions of microRNAs and protein-coding genes by gene/genome duplications in early vertebrates. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2009, 312B, 164-170.	1.3	12
33	Evolution of RNases in leaf monkeys: Being parallel gene duplications or parallel gene conversions is a problem of molecular phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 397-400.	2.7	11
34	Origins of digestive RNases in leaf monkeys are an open question. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 610-611.	2.7	2
35	Effect of site-specific heterogeneous evolution on phylogenetic reconstruction: A simple evaluation. <i>Gene</i> , 2009, 441, 156-162.	2.2	2
36	Predicting the Proportion of Essential Genes in Mouse Duplicates Based on Biased Mouse Knockout Genes. <i>Journal of Molecular Evolution</i> , 2008, 67, 705-709.	1.8	22

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37	Tissue-driven hypothesis of genomic evolution and sequence-expression correlations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2779-2784.	7.1	73
38	Tissue-driven Hypothesis with Gene Ontology (GO) Analysis. Annals of Biomedical Engineering, 2007, 35, 1088-1094.	2.5	8
39	Evolution of alternative splicing after gene duplication. Genome Research, 2006, 16, 182-189.	5.5	141
40	The Genomes of Oryza sativa: A History of Duplications. PLoS Biology, 2005, 3, e38.	5.6	808
41	EST-based Analysis of Gene Expression in the Porcine Brain. Genomics, Proteomics and Bioinformatics, 2004, 2, 237-244.	6.9	7